

KATIE SAUND

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RESEARCH

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- Scientist in Discovery Genomics at Denali Therapeutics, South San Francisco, CA 2021 - Present
- computational biology, neurodegeneration, multiomic biomarker discovery, machine learning, public datasets
- Intern with Genetics and Pharmacogenomics Department at Merck (Remote) Summer 2020
- single-cell RNA sequencing (scRNA-seq), early discovery oncology
- PhD and Postdoctoral Fellow (Promoted 2020) at University of Michigan, Ann Arbor, MI 2015 – 2021
- bacterial genomics & metagenomics, infectious disease, R software development, microbiology, evolution
- Research Assistant and Scientist I (Promoted 2014) at Seattle Children's Research Institute, Seattle, WA 2012 – 2015
- immunotherapy, solid tumor microenvironment, immuno-oncology, metabolism, NK cells & macrophages
- Research Assistant at Project Peanut Butter, Blantyre, Malawi 2010 – 2011
- food & clinical interventions for pediatric malnutrition resolution
- Research Fellow at Wayne State University, Detroit, MI 2009
- 16s rRNA alignment algorithm improvement, phylogenetic trees

EDUCATION

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- PhD in Microbiology & Immunology at University of Michigan, Ann Arbor, MI 2015 – 2020
- Awards: ASM Travel Award (2019), UM Rackham Conference Travel Grant (2019) & Professional Development Award (2019), NIH Predoctoral Genetics Training Grant (2016 – 2018), UM Maas Fellowship (2015).
 - Roles: Wolverine Venture Fund, Undergraduate Honors Thesis Research Mentor
- BS in Biology at California Institute of Technology, Pasadena, CA 2008 – 2012
- Awards: Everhart Service (2012), Teruggi Memorial (2011), Studenski Memorial (2010), & Shepard (2009).
 - Leadership: Co-President for Class of 2012.

PUBLICATIONS, PUBLICLY AVAILABLE SOFTWARE, & ORAL PRESENTATIONS

Select Publications:

- [Saund & Snitkin](#). Microbial Genomics. 2020.
- [Saund*, Lapp*, Thiede*, Pirani, Snitkin](#). Microbial Genomics. 2020. *Equal contribution.
- [Saund, Rao, Young, Snitkin](#). Open Forum Infectious Diseases. 2020.
- [Saund, Pirani, Lacy, Hanna, Snitkin](#). bioRxiv. 2021.

Software:

- [prewas](#). R package. Data preprocessing for bacterial GWAS.
- [hogwash](#). R package. Three bacterial GWAS methods.
- [snitkitr](#). R package. Data analysis tools for bacterial genomics.

Oral Presentations:

- ASM Microbe (2019)
- NIAID Systems Biology and Antibacterial Resistance Program (2018)

COMPUTATIONAL AND LABORATORY SKILLS

Computational: R, bash, package development, cloud computing (AWS: EC2, S3, ECR. Google Cloud), Terra platform, docker, high performance cluster (HPC) computing & batch scheduling (PBS, Slurm, Grid Engine), version control (git), data visualization, markdown, unit testing, linux/mac/PC, conda, machine learning, transcriptomics, genomics

Laboratory: CRISPR/Cas9 genome editing, cryostat, ELISA, experimental design, flow cytometry, immune cell isolation (cell sorting, magnetic enrichment), lentiviral transduction, mammalian cell culture, molecular biology (Gibson assembly, transfection, Western blot, qPCR), mouse handling: experimental autoimmune encephalomyelitis (multiple sclerosis mouse model), microbial techniques (anaerobic bacterial culture, bacterial stains), plasmid construction, protein co-immunoprecipitation, robotic pipetting system